Genetic variation in *Nassella neesiana* (Chilean needlegrass) in Australia

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Introduction

Chilean needlegrass (*Nassella neesiana* Trin. & Rupr.) is a noxious weed of Australia. It is a tufted perennial of the Poaceae and is capable of reproducing at an alarming rate (McLaren *et al.* 1998). Once established in an area and allowed to set seed, Chilean needlegrass cannot be completely eradicated (Storrie and Gardener 1998). Several varieties of Chilean needlegrass exist in South America (Torres 1993). *Nassella neesiana* subsp. *neesiana* has been recorded in Australia (Walsh and Entwistle 1994) but subspecies *Nassella neesiana* subsp. *gracillor* Bukart and *Nassella neesiana* subsp. *longiaristata* Arech. have not. The variety or varieties of Chilean needlegrass in Australia are unknown. The aim of this study was to examine the genetic variation in six Australian Chilean needlegrass populations across its range, by PCR-RFLP and sequencing of the internal transcribed spacer (ITS) region of ribosomal DNA (rDNA) and by RAPDs.

Results and discussion

The ITS region, amplified using the primers ITS1 and ITS4 (White *et al*. 1990), was 650 bp for all populations. The ITS-RFLP patterns with six endonuclease enzymes (*Eco*RI, *Taq*I, *Hha*I, *Hinf*I, *Hind*III and *Hae*III) were also uniform in all populations. However, sequencing showed nucleotide differences across the populations. Sequences were uniform within populations but varied between populations and did not group by geographical proximity of populations (Figure 1).

RAPD analysis using six OPA primers (Operon) was performed on the 90 DNA extracts by the method of Hsiao *et al*. (1993). Identical banding patterns were found within populations but different banding patterns were found between populations. Banding patterns were analysed by a RAPD Distance program. The distance tree grouped populations but did not show the same groupings as did the ITS sequencing (Figure 2).

Chilean needlegrass populations in Australia vary genetically between populations but are uniform within populations. This suggests that local populations are clonally propagated from cleistogenes or arise from seeds that are wind-pollinated only by local pollen. The large genetic variation found in only six provenances emphasizes the need to use a large number of provenances in testing putative biological control agents.

References

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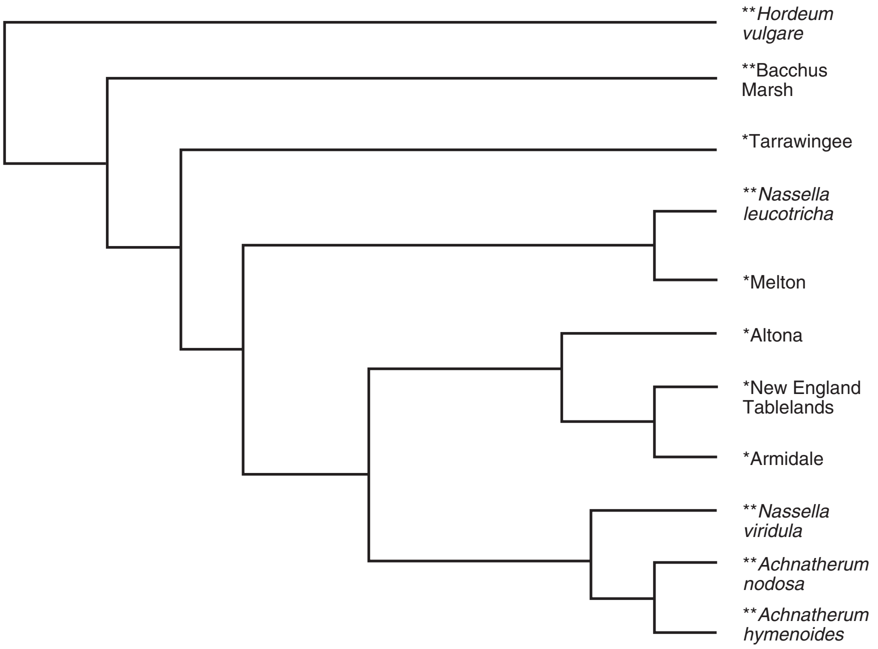

Figure 1. Relationships between populations on phylogenetic tree from ITS sequencing (* current study, ** from Phyllip on ANGIS).

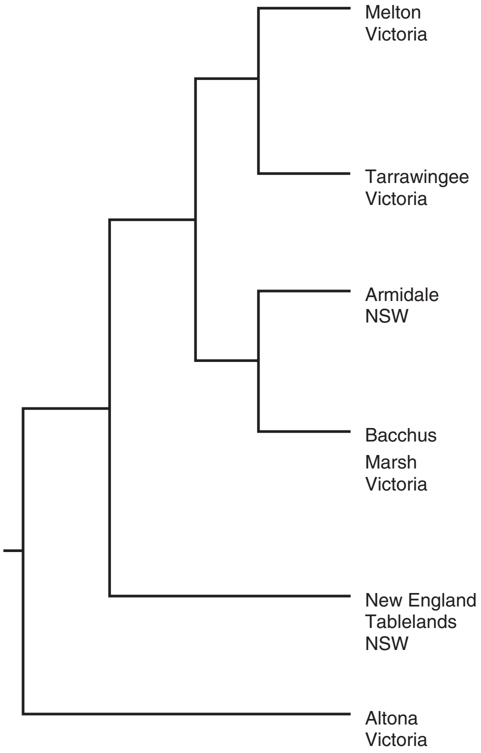

Figure 2. Relationships between and within populations by RAPD Distance.